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piece 1, NC\_000913, coaE\_guaC-, config: linear, direction: -, begin: 113473, end: 113200

This figure displays the genomic sequence of the NC\_000913.guaC gene. The top part shows the DNA sequence with various genes and their start sites indicated by asterisks (\*). The bottom part shows the corresponding RNA sequence with predicted secondary structure elements represented by red dots and lines. The structure includes several hairpins and a long terminal hairpin at the 3' end. Gene annotations are color-coded: tRNA genes are in green, rRNA genes in blue, and protein-coding genes in pink. The 5' and 3' ends of the RNA are indicated on the left and right respectively.

Sequence alignment showing the amino acid sequence of a protein. The sequence starts with fMet and ends with trp. A red dot highlights a mutation at position 113380. A purple box labeled "p35 5.6 bits" indicates a local alignment score.

~~4461~~ p35 5.6 bits

... sd

{ } p35-(26)-p10 113322 Gap 3.7 bits  
p35-p10 113322 total 7 7 bits

The diagram illustrates the 113310 mRNA sequence with various start sites indicated by red dots and different reading frames shown as colored arrows (green, blue, purple). The predicted proteins are labeled below the arrows. A green box highlights the start site at position 113310, which encodes a protein starting with fMet-ser-glu-arg-phe-ile-asn-phe-ala-phe-val-his-ser-phe-leu-thr-phe. A blue box highlights the start site at position 113300, which encodes a protein starting with fMet. A purple box highlights the start site at position 113290, which encodes a protein starting with phe. The reading frame for the first protein ends at position 113280, and the second protein starts at position 113280. The third protein starts at position 113270, and the fourth protein starts at position 113260. The fifth protein starts at position 113250, and the sixth protein starts at position 113240. The sequence continues with several other start sites indicated by red dots.

A colorful illustration of a caterpillar with a dashed line above it.

{-----} sd-(7)-ir 113304 Gap 3.7 bits  
 {-----} sd-ir 113304 coaE\_guaC- total 5.9 bits

The diagram illustrates a sequence of bits. A blue bar at the top represents the sequence from p35-(23)-p10 to p10. Below it, a green bar represents the sequence from p35-p10 to p10. The bits are color-coded: red for p35-(23), orange for p10, and green for the remaining bits. A dashed line indicates a gap between the p35-p10 and p10 segments. The total length is labeled as 4.6 bits.

p10 2.5 bits

{-----} p35-(26)-p10 113251 Gap 3.7 bit  
|-----| p35-p10 113251 total 4.1 bits

p35-p10 113251 to  
 p35 5.6 bits

Figure 1. Schematic diagram of the experimental setup. The top panel shows the optical bench with the laser source (L), beam splitter (BS), lenses (L1-L4), mirrors (M1-M4), polarizers (P1-P2), and photodetectors (PD1-PD4). The bottom panel shows the optical circuitry for the two-photon interference experiment, including the beam splitter (BS), lenses (L1-L4), mirrors (M1-M4), polarizers (P1-P2), and photodetectors (PD1-PD4).

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[-----] ... NC\_000913.coaE

The diagram illustrates the promoter region of the *coaE\_guaC* operon. It features a red box representing the *coaE* gene, a green box representing the *guaC* gene, and a blue box representing the *sd* (σ<sub>d</sub>) promoter. A dashed black line indicates the transcription start site. Two sets of arrows above the line represent transcription direction: red arrows pointing left (from the *sd* promoter) and green arrows pointing right (from the *coaE* gene). A green bracket below the genes indicates a gap of 3.0 bits between the *sd* promoter and the *coaE* gene. Another bracket below shows the total length of 12.6 bits for the entire *sd-coaE-guaC* construct.

p10 2.2 bits

... --> p35-(24)-p10 113229 Gap 2.4 bits  
... --> p35-p10 113229 total 5.4 bits